SEQUENCE LISTING

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<120> CD8 AS AN INHIBITOR OF THE CELLULAR IMMUNE SYSTEM

<130> 102286.413

<140> US 09/560,494
<141> 2000-04-28

<150> PCT/GB98/03235
<151> 1998-10-28

<150> GB 9722779.7
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<220>
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<400> 2
tattcgactg gatccttata cgtatctcgc cgaaaggctg gg 42

<210> 3
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<213> Artificial Sequence

<220>
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<400> 3
ggaattccat atgagccagt tccgggtgtc gccgctggat cg 42

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<211> 59
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<213> Artificial Sequence

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<223> Synthetic DNA primer

<400> 6
caccgcgaat tcggatccta agcgggtcta caagcttctg gcgtcgtggt gggcttcgc 59

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<220>
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<400> 7
caccgcgaat tcggatccta agcgggtcta caagcttcgg gcttcgctgg caggaagacc 60

<210> 8
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA primer

<400> 8
gtggcaagct tggatcctat ggcgtcgtgg tgggcttcgc tg 42

<210> 9
<211> 42
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<223> Synthetic DNA primer

<400> 9
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<212> DNA
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<223> Synthetic DNA primer

<400> 10
acatacccat gggctctcac tccatgaggt atttc 35

<210> 11
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<400> 11
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<210> 12
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<212> PRT
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<220>
<223> HLA-A2 Pol-restricted CTL line specific peptide

<400> 12
Ile Leu Lys Glu Pro Val His Gly Val
1 5

<210> 13
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A2 Pol-restricted CTL line specific peptide

<400> 13
Ser Leu Tyr Asn Thr Val Ala Thr Leu
1 5

<210> 14
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> HLA-A2 Pol-restricted CTL line specific peptide

<400> 14
Val Ile Tyr Gln Tyr Met Asp Asp Leu
1 5

<210> 15
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA primer

<400> 15
ctgtccaacc cgacgtcggg cagctcgtgg ctcttccagc cg 42

<210> 16
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA primer

<400> 16
cggctggaag agccacgagc tgcccgacgt cgggttggac ag 42

<210> 17
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<220>
<223> Synthetic DNA primer

<400> 17
gggggaagct taatgccatt cgattttctg agcttcaaaa atatcgttca gaccaccacc 60
ggatcctggc gtcgtggtgg gcttcgctgg caggaagac 99

<210> 18
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<212> PRT
<213> Artificial Sequence

<220>
<223> CD8 alpha polypeptide

<400> 18
Gly Ser Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu
1 5 10 15
Trp His

<210> 19
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA primer

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gcc 63

<210> 20
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA primer

<400> 20
ggggagggaa gcttacttgg tagtagtaga gttcac 36

<210> 21
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A2-flu

<400> 21
Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5

<210> 22
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide epitope

<400> 22
Lys Ala Val Tyr Asn Phe Ala Thr Cys
1 5

<210> 23
<211> 366
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<213> Artificial Sequence

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<223> synthetic DNA construct encoding part of the
extracellular domain of human CD8 alpha

<221> CDS

<222> (1)...(366)

<400> 23

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 1               5                  10                  15

gag aca gtg gag ctg aag tgc cag gtg ctg ctg tcc aac ccg acg tcg   96
Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser Asn Pro Thr Ser
            20                  25                  30

ggc tgc tcg tgg ctc ttc cag ccg cgc ggc gcc gcc gcc agt ccc acc  144
Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala Ala Ser Pro Thr
        35                  40                  45

ttc ctc cta tac ctc tcc caa aac aag ccc aag gcg gcc gag ggg ctg  192
Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala Ala Glu Gly Leu
    50                  55                  60

gac acc cag cgg ttc tcg ggc aag agg ttg ggg gac acc ttc gtc ctc  240
Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp Thr Phe Val Leu
65                  70                  75                  80

acc ctg agc gac ttc cgc cga gag aac gag ggc tac tat ttc tgc tcg  288
Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr Tyr Phe Cys Ser
                85                  90                  95

gcc ctg agc aac tcc atc atg tac ttc agc cac ttc gtg ccg gtc ttc  336
Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe
            100                 105                 110

ctg cca gcg aag ccc acc acg acg cca tag                          366
Leu Pro Ala Lys Pro Thr Thr Thr Pro  *
        115                 120
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<210> 24
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> an amino acid construct encoding part of the
extracellular domain of human CD8 alpha

<400> 24

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Met Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr Trp Asn Leu Gly
 1               5                  10                  15
Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser Asn Pro Thr Ser
            20                  25                  30
Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala Ala Ser Pro Thr
        35                  40                  45
Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala Ala Glu Gly Leu
    50                  55                  60
Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp Thr Phe Val Leu
65                  70                  75                  80
Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr Tyr Phe Cys Ser
                85                  90                  95
Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val Pro Val Phe
```

```
           100                 105                 110
Leu Pro Ala Lys Pro Thr Thr Thr Pro
        115                 120
```

<210> 25
<211> 400
<212> DNA
<213> Artificial Sequence

<220>
<223> a synthetic DNA construct encoding part of the
extracellular domain of murine CD8 alpha

<221> CDS
<222> (4)...(396)

<400> 25

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cat atg aaa cca caa gca cct gaa cta cga atc ttt cca aag aaa atg   48
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     1               5                  10                  15

gac gcc gaa ctt ggt cag aag gtg gac ctg gta tgt gaa gtg ttg ggg   96
Asp Ala Glu Leu Gly Gln Lys Val Asp Leu Val Cys Glu Val Leu Gly
                20                  25                  30

tcc gtt tcg caa gga tgc tct tgg ctc ttc cag aac tcc agc tcc aaa   144
Ser Val Ser Gln Gly Cys Ser Trp Leu Phe Gln Asn Ser Ser Ser Lys
            35                  40                  45

ctc ccc cag ccc acc ttc gtt gtc tat atg gct tca tcc cac aac aag   192
Leu Pro Gln Pro Thr Phe Val Val Tyr Met Ala Ser Ser His Asn Lys
        50                  55                  60

ata acg tgg gac gag aag ctg aat tcg tcg aaa ctg ttt tct gcc atg   240
Ile Thr Trp Asp Glu Lys Leu Asn Ser Ser Lys Leu Phe Ser Ala Met
    65                  70                  75

agg gac acg aat aat aag tac gtt ctc acc ctg aac aag ttc agc aag   288
Arg Asp Thr Asn Asn Lys Tyr Val Leu Thr Leu Asn Lys Phe Ser Lys
80                  85                  90                  95

gaa aac gaa ggc tac tat ttc tgc tca gtc atc agc aac tcg gtg atg   336
Glu Asn Glu Gly Tyr Tyr Phe Cys Ser Val Ile Ser Asn Ser Val Met
                100                 105                 110

tac ttc agt tct gtc gtg cca gtc ctt cag aaa gtg aac tct act act   384
Tyr Phe Ser Ser Val Val Pro Val Leu Gln Lys Val Asn Ser Thr Thr
            115                 120                 125

acc aag cca taa gctt                                             400
Thr Lys Pro  *
        130
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<210> 26
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> an amino acid construct encoding part of the
extracelular domain of murine CD8 alpha

<400> 26
Met Lys Pro Gln Ala Pro Glu Leu Arg Ile Phe Pro Lys Lys Met Asp
1 5 10 15
Ala Glu Leu Gly Gln Lys Val Asp Leu Val Cys Glu Val Leu Gly Ser
20 25 30
Val Ser Gln Gly Cys Ser Trp Leu Phe Gln Asn Ser Ser Ser Lys Leu
35 40 45
Pro Gln Pro Thr Phe Val Val Tyr Met Ala Ser Ser His Asn Lys Ile
50 55 60
Thr Trp Asp Glu Lys Leu Asn Ser Ser Lys Leu Phe Ser Ala Met Arg
65 70 75 80
Asp Thr Asn Asn Lys Tyr Val Leu Thr Leu Asn Lys Phe Ser Lys Glu
85 90 95
Asn Glu Gly Tyr Tyr Phe Cys Ser Val Ile Ser Asn Ser Val Met Tyr
100 105 110
Phe Ser Ser Val Val Pro Val Leu Gln Lys Val Asn Ser Thr Thr Thr
115 120 125
Lys Pro
130

<210> 27
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8 protein

<400> 27
Leu Leu Leu His Ala Ala Arg Pro
1 5

<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CD8 protein

<400> 28
Ala Pro Arg Pro Pro Thr Pro Ala
1 5

<210> 29
<211> 708
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(708)
<223> Human CD8 alpha

<221> CDS
<222> (1)...(708)

<400> 29

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atg gcc tta cca gtg acc gcc ttg ctc ctg ccg ctg gcc ttg ctg ctc   48
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1               5                  10                  15

cac gcc gcc agg ccg agc cag ttc cgg gtg tcg ccg ctg gat cgg acc   96
His Ala Ala Arg Pro Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr
            20                  25                  30

tgg aac ctg ggc gag aca gtg gag ctg aag tgc cag gtg ctg ctg tcc   144
Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser
        35                  40                  45

aac ccg acg tcg ggc tgc tcg tgg ctc ttc cag ccg cgc ggc gcc gcc   192
Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
    50                  55                  60

gcc agt ccc acc ttc ctc cta tac ctc tcc caa aac aag ccc aag gcg   240
Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
65                  70                  75                  80

gcc gag ggg ctg gac acc cag cgg ttc tcg ggc aag agg ttg ggg gac   288
Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
                85                  90                  95

acc ttc gtc ctc acc ctg agc gac ttc cgc cga gag aac gag ggc tac   336
Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
            100                 105                 110

tat ttc tgc tcg gcc ctg agc aac tcc atc atg tac ttc agc cac ttc   384
Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
        115                 120                 125

gtg ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga   432
Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg
    130                 135                 140

cca cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc   480
Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
145                 150                 155                 160

cca gag gcg tgc cgg cca gcg gcg ggg ggc gca gtg cac acg agg ggg   528
Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
                165                 170                 175

ctg gac ttc gcc tgt gat atc tac atc tgg gcg ccc ttg gcc ggg act   576
Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
            180                 185                 190

tgt ggg gtc ctt ctc ctg tca ctg gtt atc acc ctt tac tgc aac cac   624
Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His
        195                 200                 205

agg aac cga aga cgt gtt tgc aaa tgt ccc cgg cct gtg gtc aaa tcg   672
Arg Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser
    210                 215                 220
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gga gac aag ccc agc ctt tcg gcg aga tac gtc taa                    708
Gly Asp Lys Pro Ser Leu Ser Ala Arg Tyr Val  *
225                 230                 235
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<210> 30
<211> 235
<212> PRT
<213> Homo sapien

<400> 30

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Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1               5                  10                  15
His Ala Ala Arg Pro Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr
            20                  25                  30
Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser
        35                  40                  45
Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
    50                  55                  60
Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
65                  70                  75                  80
Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
                85                  90                  95
Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
            100                 105                 110
Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
        115                 120                 125
Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg
    130                 135                 140
Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
145                 150                 155                 160
Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
                165                 170                 175
Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
            180                 185                 190
Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His
        195                 200                 205
Arg Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser
    210                 215                 220
Gly Asp Lys Pro Ser Leu Ser Ala Arg Tyr Val
225                 230                 235
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